

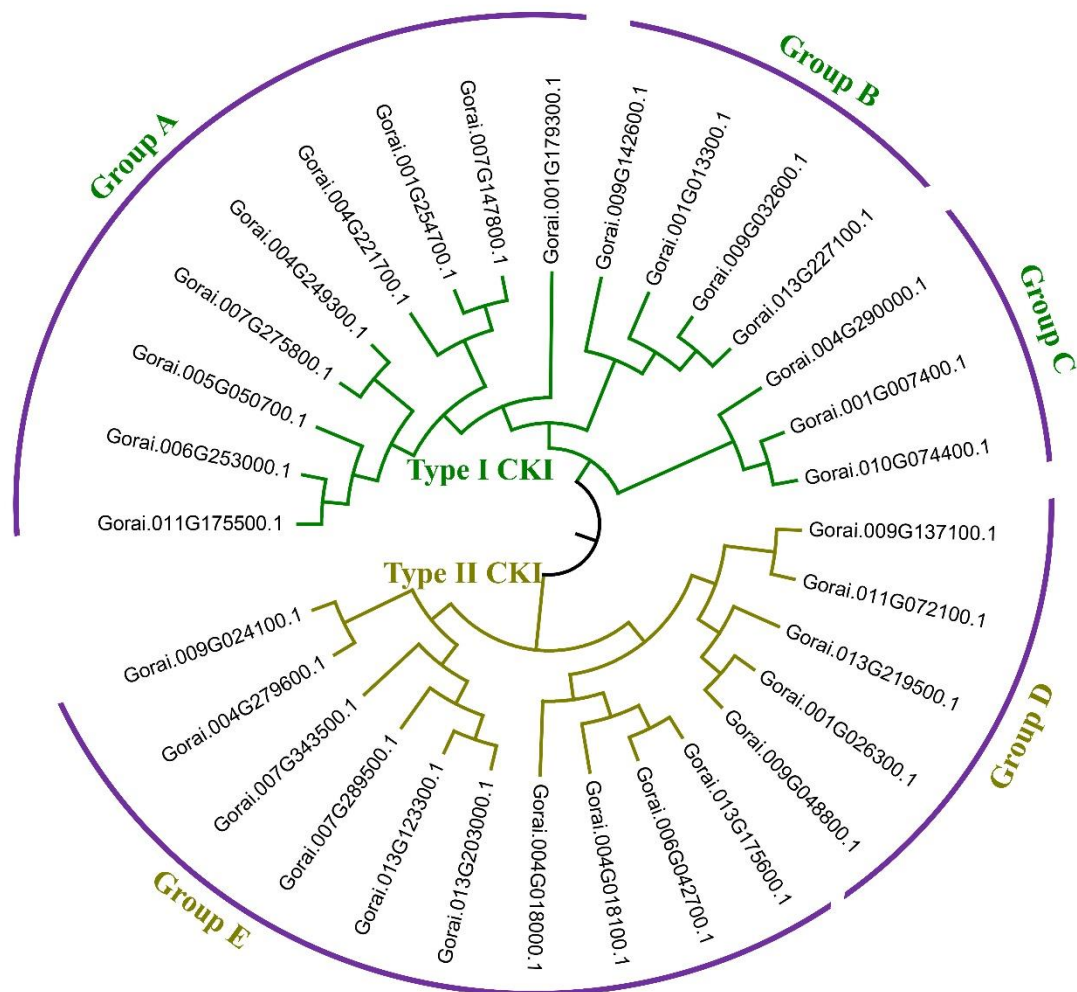


Figure S1. Phylogenetic analyses of CKI gene family in *G. raimondii*.

Amino acid sequences were aligned using ClustalX and the phylogenetic tree was constructed using 31 protein sequence from *G. raimondii* by the maximum likelihood method in MEGA 6 software. GrCKI proteins were divided into two types: type I and type II. The type I GrCKI proteins were divided into three subclasses: Group A (9 genes), B (4 genes) and C (3 genes). The type II GrCKI proteins included two subclasses: Group D (5 genes) and E (10 genes). The GeneID of type I and type II *GrCKI* genes were listed in Table S1.

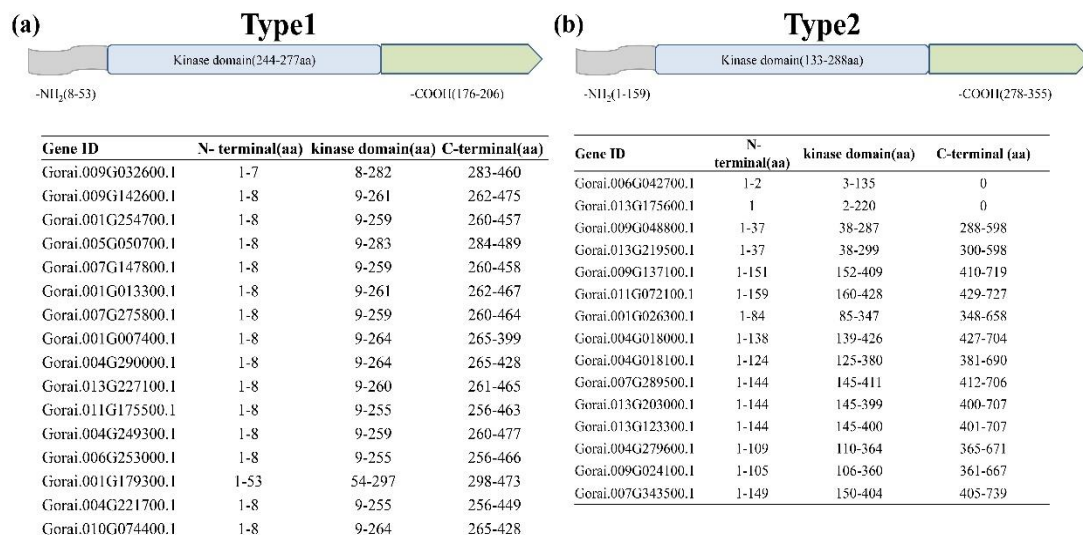


Figure S2. Structural analysis of the *CKI* genes in *G. raimondii*.

(a) and (b) Structural analysis of the type I and type II GrCKI proteins, respectively.

The putative conserved domain of GrCKI proteins were analyzed using the online program Conserved Domain Search Service (CD Search) (<http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>). The GrCKI proteins are highly conserved kinase domain, but differ significantly in the length and primary structure of their N-terminal and C-terminal domains.

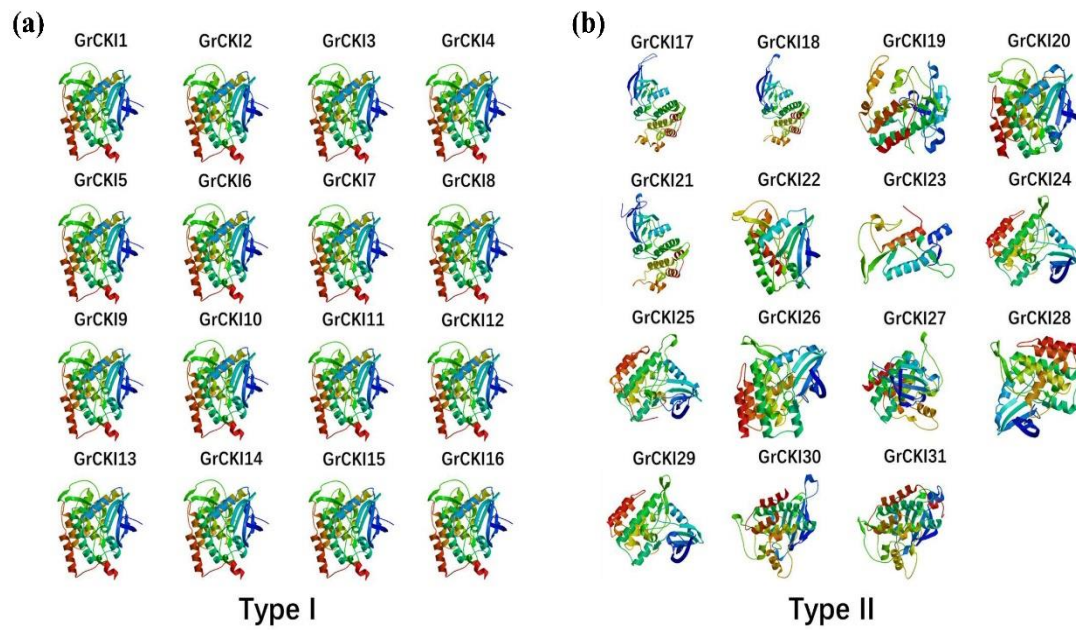


Figure S3. Predicted 3D structure of *GrCKI* proteins.

(a) and (b) Predicted 3D structural analysis of the type I GrCKIs (16 genes) and type II GrCKIs (15 genes), respectively. 3D structure was predicted by SWISS-MODEL ([https:// swissmodel.expasy.org/](https://swissmodel.expasy.org/)) using 31 protein sequences from *G.raimondii*.

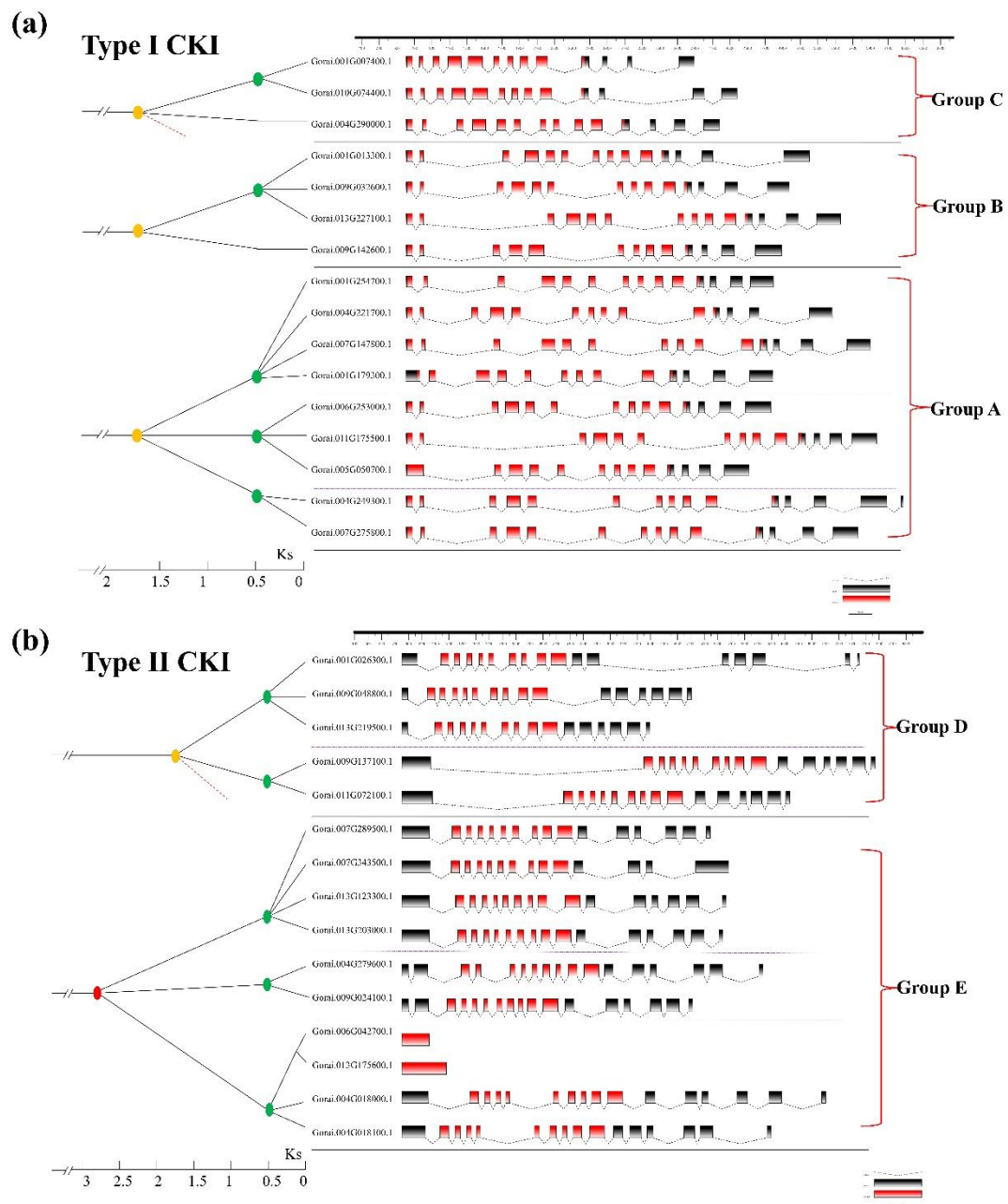


Figure S4. Exon/Intron organization of the *CKI* genes in *G. raimondii*.

(a) and (b) Exon/intron structures of the type I and type II *CKI* genes in *G. raimondii*, respectively. The type I *GrCKI* genes were divided into three subclasses: Group A (9 genes), B (4 genes) and C (3 genes). The type II *GrCKI* genes were divided into two subclasses: Group D (5 genes) and E (10 genes). Boxes denote exons within coding regions, and the dash lines connecting them represent introns. Solid red boxes show the kinase domains.

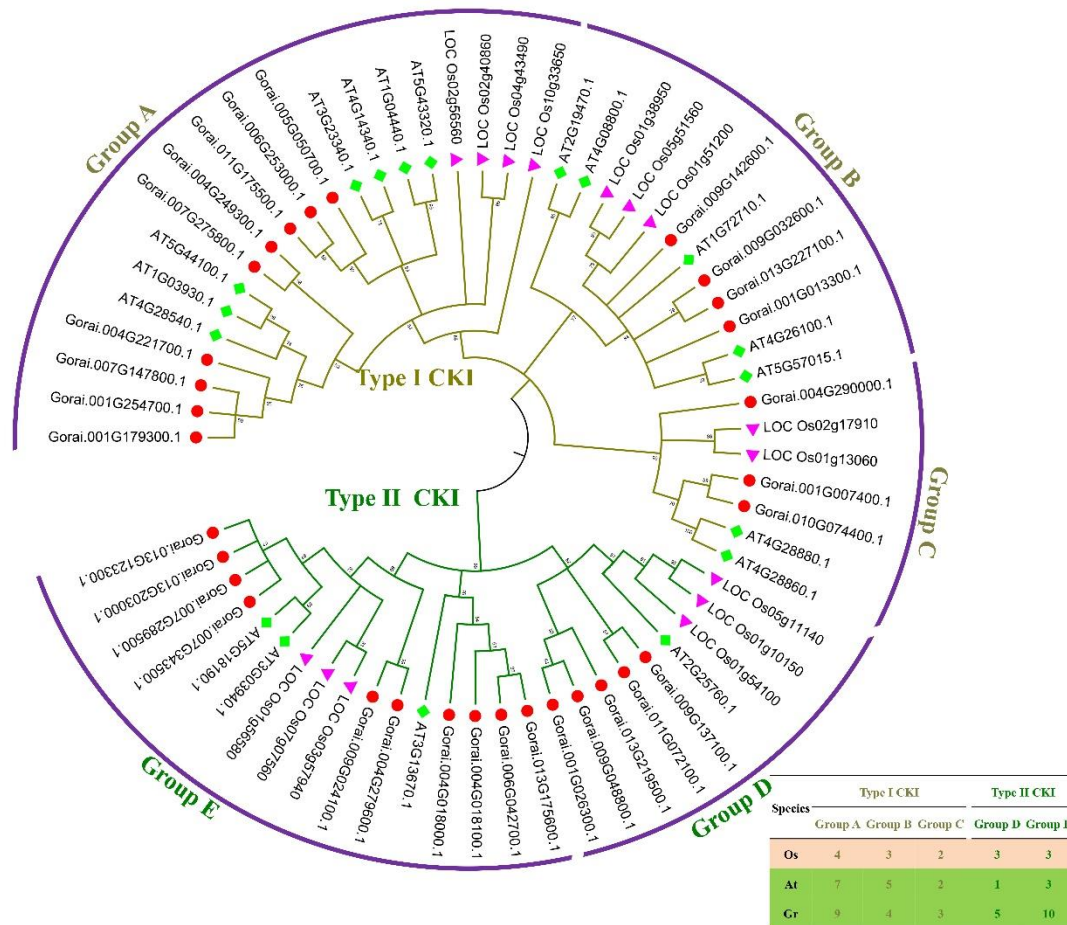


Figure S5. Phylogenetic analyses of *CKI* gene family in eudicot (*A. thaliana*, *G. raimondii*) and monocot (*O. sativa*). Amino acid sequences were aligned using ClustalX and the phylogenetic tree was conducted using MEGA 6 software with the maximum likelihood method. Three different symbols were represented for *G. raimondii*, *A. thaliana* and *O. sativa*, respectively. The Gene ID of type I and type II *CKI* genes from *G. raimondii*, *A. thaliana* and *O. sativa* were listed in Table S1.

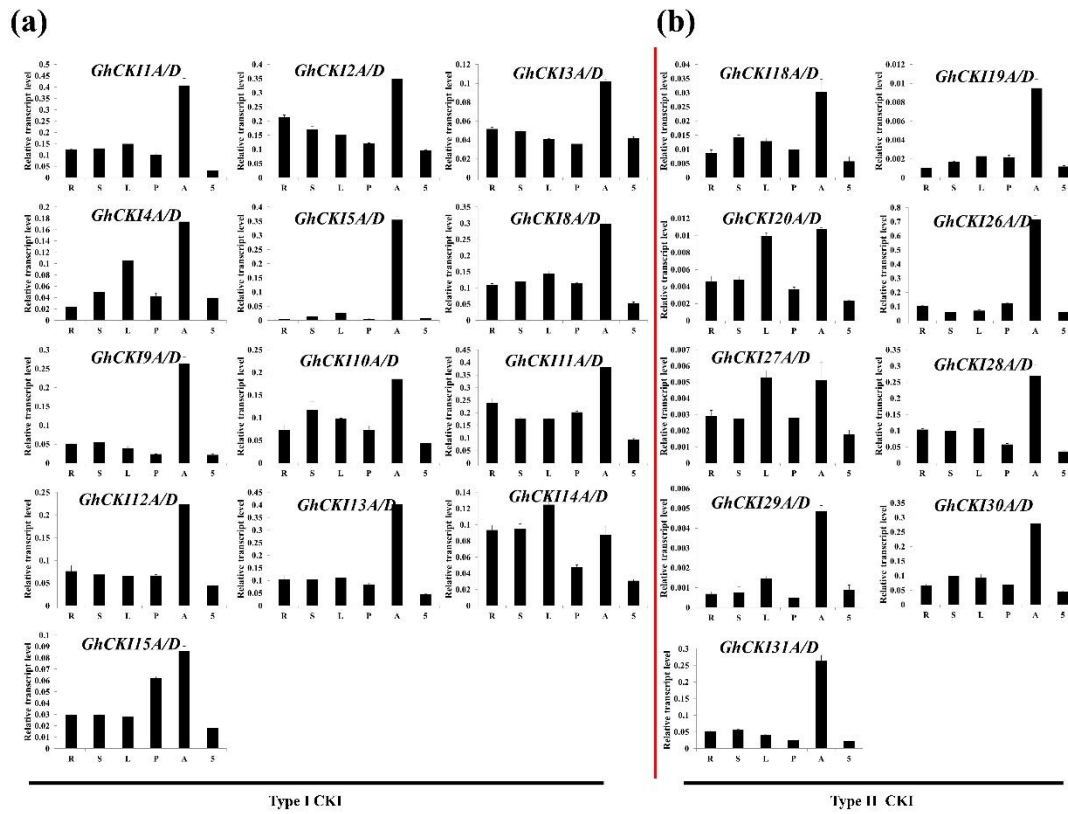


Figure S6. Quantitative RT-PCR analysis of the expression of *G. hirsutum* CKI genes in upland cotton tissues.

(a) and (b) Expression profiles of the type I *GhCKI* genes (26 genes) and type II *GhCKI* genes (18 genes) in upland cotton tissues, respectively. R, root; S, shoot; L, leaves; P, petal; A, anther; and 5, ovules at 5 days post-anthesis (DPA). The GeneID of type I and type II *GhCKI* genes was listed in Table 1.

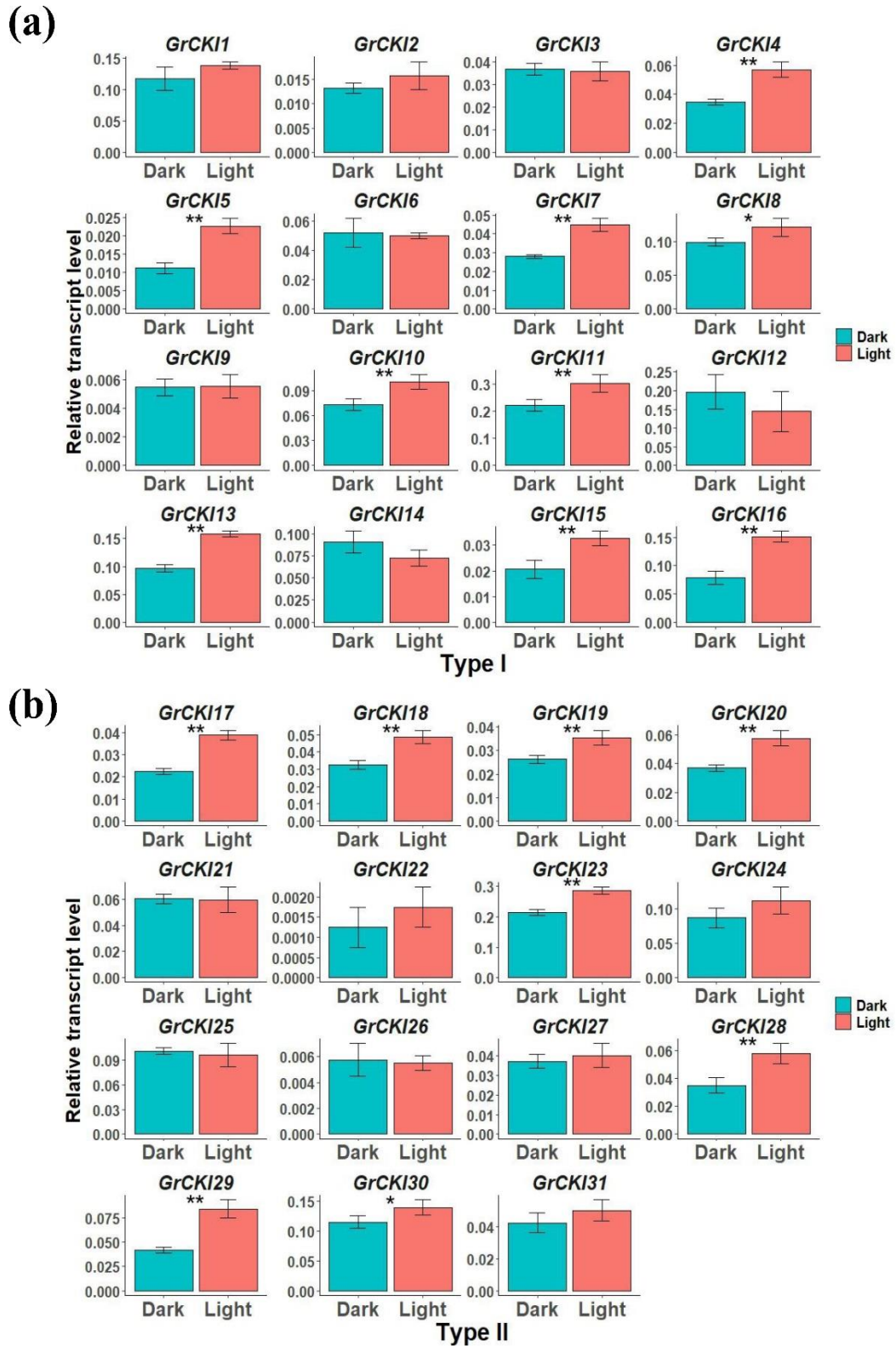


Figure S7. Expression profiles of *CKI* genes under dark and light condition in *G. raimondii*.

(a) and (b) Expression profiles of the type I *GrCKI* genes (16 genes) and the type II

GrCKI genes (15 genes) in cotyledon from *G. raimondii* under light and dark conditions.

Error bars indicate $\pm$ standard deviations of triplicate experiments. Asterisks indicate statistically significant differences (* $P < 0.05$, ** $P < 0.01$) by Student's *t* test. *GrUB7* gene was used as the reference gene to normalize the total amount of cDNA in each reaction.